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SEQUENCE LISTING

<110> Haseltine et al.

<120> Human DNA Mismatch Repair Proteins

<130> PF106P3D1

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<141> 2002-02-22

<150> PCT/US95/01035

<151> 1995-01-25

<150> 08/468,024

<151> 1995-06-06

<150> 08/465,679

<151> 1995-06-06

<150> 08/294,312

<151> 1994-08-23

<150> 08/210,143

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<150> 08/187,757

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	ttc tat gga gta gca gat tta aaa gaa att ctt aat gct ata tta aac			2657
	Phe Tyr Gly Val Ala Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn			
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	Arg Asn Ala Lys Glu Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser			
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Thr Ala Lys Lys Cys Lys Asp Glu Ile Lys Lys Ile Gln Asp Leu Leu  
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Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg Ile Val Phe Val His  
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Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val Ser Asp His Lys Met  
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Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr Leu Ser Gly Phe Leu  
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Pro Lys Cys Asp Ala Asp His Ser Phe Thr Ser Leu Ser Thr Pro Glu  
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Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val His Gln Lys Asp Ile  
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Leu Lys Leu Ile Arg His His Tyr Asn Leu Lys Cys Leu Lys Glu Ser  
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Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala  
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 625 630 635 640

Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro  
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51

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Glu Pro Ala Lys Ala Ile Lys Pro Ile Asp Arg Lys Ser Val His Gln

99



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Ile Cys Ser Gly	Gln Val Val Leu Ser	Leu Ser Thr Ala Val	Lys Glu	
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Leu Val Glu Asn Ser Leu Asp	Ala Gly Ala Thr Asn Ile Asp	Leu Lys		
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Leu Lys Asp Tyr Gly Val Asp	Leu Ile Glu Val Ser Asp	Asn Gly Cys		
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Gly Val Glu Glu Glu Asn Phe	Glu Gly Leu Thr Leu Lys His His Thr			
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Ser Lys Ile Gln Glu Phe Ala Asp	Leu Thr Gln Val Glu Thr Phe Gly			
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Phe Arg Gly Glu Ala Leu Ser Ser Leu Cys Ala Leu Ser Asp Val Thr				
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Ile Ser Thr Cys His Ala Ser Ala Lys Val Gly Thr Arg Leu Met Phe				
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Asp His Asn Gly Lys Ile Ile Gln Lys Thr Pro Tyr Pro Arg Pro Arg				
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Gly Thr Thr Val Ser Val Gln Gln Leu Phe Ser Thr Leu Pro Val Arg				
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Gln Val Leu His Ala Tyr Cys Ile Ile Ser Ala Gly Ile Arg Val Ser				
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Cys Thr Asn Gln Leu Gly Gln Gly Lys Arg Gln Pro Val Val Cys Thr				
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Gly Gly Ser Pro Ser Ile Lys Glu Asn Ile Gly Ser Val Phe Gly Gln				
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Lys Gln Leu Gln Ser Leu Ile Pro Phe Val Gln Leu Pro Pro Ser Asp				
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Ser Val Cys Glu Glu Tyr Gly Leu Ser Cys Ser Asp Ala Leu His Asn				

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Leu Phe Tyr Ile Ser Gly Phe Ile Ser Gln Cys Thr His Gly Val Gly	270	275	280	
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Arg Ser Ser Thr Asp Arg Gln Phe Phe Phe Ile Asn Arg Arg Pro Cys	285	290	295	
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Asp Pro Ala Lys Val Cys Arg Leu Val Asn Glu Val Tyr His Met Tyr	300	305	310	
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Asn Arg His Gln Tyr Pro Phe Val Val Leu Asn Ile Ser Val Asp Ser	315	320	325	
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Glu Cys Val Asp Ile Asn Val Thr Pro Asp Lys Arg Gln Ile Leu Leu	330	335	340	345
caa gag gaa aag ctt ttg ttg gca gtt tta aag acc tct ttg ata gga				1107
Gln Glu Glu Lys Leu Leu Leu Ala Val Leu Lys Thr Ser Leu Ile Gly	350	355	360	
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Met Phe Asp Ser Asp Val Asn Lys Leu Asn Val Ser Gln Gln Pro Leu	365	370	375	
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Leu Asp Val Glu Gly Asn Leu Ile Lys Met His Ala Ala Asp Leu Glu	380	385	390	
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Lys Pro Met Val Glu Lys Gln Asp Gln Ser Pro Ser Leu Arg Thr Gly	395	400	405	
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Glu Glu Lys Lys Asp Val Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser	410	415	420	425
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Leu Arg His Thr Thr Glu Asn Lys Pro His Ser Pro Lys Thr Pro Glu	430	435	440	
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Pro Arg Arg Ser Pro Leu Gly Gln Lys Arg Gly Met Leu Ser Ser Ser	445	450	455	
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Thr Ser Gly Ala Ile Ser Asp Lys Gly Val Leu Arg Pro Gln Lys Glu	460	465	470	
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Ala Val Ser Ser Ser His Gly Pro Ser Asp Pro Thr Asp Arg Ala Glu	475	480	485	
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Val Glu Lys Asp Ser Gly His Gly Ser Thr Ser Val Asp Ser Glu Gly				

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Gln His Thr Val Leu Gln Gly Gln Arg Leu Ile Ala Pro Gln Thr Leu							
		715		720		725	
aac tta act gct gtt aat gaa gct gtt ctg ata gaa aat ctg gaa ata	2259						
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750		755	760	
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765		770	775	
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Phe Gly Pro Gln Asp Val Asp Glu Leu Ile Phe Met Leu Ser Asp Ser				
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Pro Gly Val Met Cys Arg Pro Ser Arg Val Lys Gln Met Phe Ala Ser				
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Arg Ala Cys Arg Lys Ser Val Met Ile Gly Thr Ala Leu Asn Thr Ser				
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Glu Met Lys Lys Leu Ile Thr His Met Gly Glu Met Asp His Pro Trp				
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Asn Cys Pro His Gly Arg Pro Thr Met Arg His Ile Ala Asn Leu Gly				
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Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
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Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Ala Ser  
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Ala Lys Val Gly Thr Arg Leu Met Phe Asp His Asn Gly Lys Ile Ile  
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Gln Leu Phe Ser Thr Leu Pro Val Arg His Lys Glu Phe Gln Arg Asn  
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Ile Lys Lys Glu Tyr Ala Lys Met Val Gln Val Leu His Ala Tyr Cys  
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Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys  
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Ile Ser Gln Cys Thr His Gly Val Gly Arg Ser Ser Thr Asp Arg Gln  
 275 280 285

Phe Phe Phe Ile Asn Arg Arg Pro Cys Asp Pro Ala Lys Val Cys Arg  
 290 295 300

Leu Val Asn Glu Val Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe  
 305 310 315 320

Val Val Leu Asn Ile Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val  
 325 330 335

Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu  
 340 345 350

Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Val Asn  
 355 360 365

Lys Leu Asn Val Ser Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu  
 370 375 380

Ile Lys Met His Ala Ala Asp Leu Glu Lys Pro Met Val Glu Lys Gln  
 385 390 395 400

Asp Gln Ser Pro Ser Leu Arg Thr Gly Glu Glu Lys Lys Asp Val Ser  
 405 410 415

Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu Arg His Thr Thr Glu Asn  
 420 425 430

Lys Pro His Ser Pro Lys Thr Pro Glu Pro Arg Arg Ser Pro Leu Gly  
 435 440 445

Gln Lys Arg Gly Met Leu Ser Ser Ser Thr Ser Gly Ala Ile Ser Asp  
 450 455 460

Lys Gly Val Leu Arg Pro Gln Lys Glu Ala Val Ser Ser Ser His Gly  
 465 470 475 480

Pro Ser Asp Pro Thr Asp Arg Ala Glu Val Glu Lys Asp Ser Gly His  
 485 490 495

Gly Ser Thr Ser Val Asp Ser Glu Gly Phe Ser Ile Pro Asp Thr Gly  
 500 505 510

Ser His Cys Ser Ser Glu Tyr Ala Ala Ser Ser Pro Gly Asp Arg Gly  
 515 520 525

Ser Gln Glu His Val Asp Ser Gln Glu Lys Ala Pro Glu Thr Asp Asp  
530 535 540

Ser Phe Ser Asp Val Asp Cys His Ser Asn Gln Glu Asp Thr Gly Cys  
545 550 555 560

Lys Phe Arg Val Leu Pro Gln Pro Thr Asn Leu Ala Thr Pro Asn Thr  
565 570 575

Lys Arg Phe Lys Lys Glu Glu Ile Leu Ser Ser Ser Asp Ile Cys Gln  
580 585 590

Lys Leu Val Asn Thr Gln Asp Met Ser Ala Ser Gln Val Asp Val Ala  
595 600 605

Val Lys Ile Asn Lys Lys Val Val Pro Leu Asp Phe Ser Met Ser Ser  
610 615 620

Leu Ala Lys Arg Ile Lys Gln Leu His His Glu Ala Gln Gln Ser Glu  
625 630 635 640

Gly Glu Gln Asn Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu  
645 650 655

Asn Gln Ala Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Thr Met  
660 665 670

Phe Ala Glu Met Glu Ile Ile Gly Gln Phe Asn Leu Gly Phe Ile Ile  
675 680 685

Thr Lys Leu Asn Glu Asp Ile Phe Ile Val Asp Gln His Ala Thr Asp  
690 695 700

Glu Lys Tyr Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Gly  
705 710 715 720

Gln Arg Leu Ile Ala Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu  
725 730 735

Ala Val Leu Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp  
740 745 750

Phe Val Ile Asp Glu Asn Ala Pro Val Thr Glu Arg Ala Lys Leu Ile  
755 760 765

Ser Leu Pro Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Val Asp  
 770 775 780

Glu Leu Ile Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro  
 785 790 795 800

Ser Arg Val Lys Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val  
 805 810 815

Met Ile Gly Thr Ala Leu Asn Thr Ser Glu Met Lys Lys Leu Ile Thr  
 820 825 830

His Met Gly Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro  
 835 840 845

Thr Met Arg His Ile Ala Asn Leu Gly Val Ile Ser Gln Asn  
 850 855 860

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<220>  
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<400> 7  
 gttgaacatc tagacgtctc 20

<210> 8  
 <211> 19  
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<220>  
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<400> 8  
 tcgtggcagg ggattattcg 19

<210> 9  
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 <212> DNA  
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<400> 9  
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<210> 10  
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22

<210> 11  
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<220>  
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<400> 11  
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18

<210> 12  
<211> 19  
<212> DNA  
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<220>  
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<400> 12  
gggctgtgtg aatcctcag

19

<210> 13  
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<212> DNA  
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<220>  
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<400> 13  
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20

<210> 14  
<211> 18  
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<220>  
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<400> 14  
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18

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<212> DNA  
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20

<210> 16  
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<213> Artificial Sequence  
  
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19

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<400> 17  
caacaatgta ttcagnaagt cc

22

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21

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 <400> 23  
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<223> hMLH1 sense primer

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19

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 25

ggaaatggtg gaagatgatt c

21

<210> 26

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 26

cttctcaaca ccaagc

16

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 27

gaaattgatg aggaagggaa c

21

<210> 28

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> hMLH1 sense primer

<400> 28

cttctgattg acaactatgt gc

22

<210> 29

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer  
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 <210> 30  
 <211> 20  
 <212> DNA  
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 <223> hMLH1 antisense primer  
 <400> 33  
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 <210> 34  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
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<223> hMLH1 5' primer with BamHI restriction site  
 <400> 34  
 cgggatccat gtcgttcgtg gcaggg 26  
 <210> 35  
 <211> 26  
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 <223> hMLH1 3' primer with XbaI restriction site  
 <400> 35  
 gctctagatt aacacctctc aaagac 26  
 <210> 36  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> hMLH1 primer useful for amplifying codons 1 to 394  
 <400> 36  
 gcatctagac gtttccttgg c 21  
 <210> 37  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> primer useful for amplifying codons 1 to 394 of hMLH1  
 <400> 37  
 catccaagct tctgttcccg 20  
 <210> 38  
 <211> 19  
 <212> DNA  
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 <223> primer useful for amplifying codons 326 to 729 of hMLH1  
 <400> 38  
 ggggtgcagc agcacatcg 19  
 <210> 39  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
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<223> primer useful for amplifying codons 326 to 729 of hMLH1  
 <400> 39  
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 <210> 40  
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 <212> DNA  
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 <400> 40  
 tcccaaagaa ggacttgct 19  
  
 <210> 41  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> primer useful for amplifying codons 602 to 756 plus 128  
 nucleotides of 3' untranslated sequence of hMLH1  
 <400> 41  
 agtataagtc ttaagtgcta cc 22  
  
 <210> 42  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer useful for amplifying codons 578 to 632 of hMLH1  
 <400> 42  
 tttatggttt ctcacctgcc 20  
  
 <210> 43  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer useful for amplifying codons 578 to 632 of hMLH1  
 <400> 43  
 gttatctgcc cacctcagc 19  
  
 <210> 44  
 <211> 59  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer useful for amplifying codons 1 to 394 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 44  
 ggatcctaatacgcactcactatagggagaccaccatggcattctagacgtttcccttggc 59

<210> 45  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer useful for amplifying codons 1 to 394 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 45  
 catccaagcttctgttcccg 20

<210> 46  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer useful for amplifying codons 326 to 729 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 46  
 ggatcctaatacgcactcactatagggagaccaccatgggggtgcagcagcacatcg 56

<210> 47  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer useful for amplifying codons 326 to 729 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 47  
 ggaggcagaa tgtgtgagcg 20

<210> 48  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> hMLH2 5' primer with a BamHI restriction site

<400> 48  
 cgggatccatgaaacaattgcctgcggc 28



<210> 49  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> hMLH2 3' primer with XbaI restriction site  
  
 <400> 49  
 gctctagacc agactcatgc tgtttt 26

<210> 50  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> hMLH3 5' primer with a BamHI restriction site  
  
 <400> 50  
 cgggatccat ggagcgagct gagagc 26

<210> 51  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> hMLH3 3' primer with XbaI restriction site  
  
 <400> 51  
 gctctagagt gaagactctg tct 23

<210> 52  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> hMLH2 primer  
  
 <400> 52  
 aagctgctct gttaaaagcg 20

<210> 53  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> hMLH2 primer  
  
 <400> 53  
 gcaccagcat ccaaggag 18

<210> 54  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> hMLH3 primer

<400> 54  
caaccatgag acacatcgc

19

<210> 55  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> hMLH3 primer

<400> 55  
aggttagtga agactctgtc

20

<210> 56  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 1 to 500 of hMLH2

<400> 56  
ggatcctaatacgcactcact atagggagac caccatggaa caattgcctg cgg

53

<210> 57  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 1 to 500 of hMLH2

<400> 57  
cctgctccac tcactctgc

18

<210> 58  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 270 to 755 of hMLH2

<400> 58  
ggatcctaatacgcactcact atagggagac caccatggaa gatattcttaa agttaatccg

60

<210> 59  
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 <212> DNA  
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 <400> 59  
 ggcttcttct actctatatg g 21  
  
 <210> 60  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer useful for amplifying from codon 485 to the translation  
 termination site at codon 933 of hMLH2  
  
 <400> 60  
 ggatcctaatac gactcact atagggagac caccatggca ggtcttgaaa actcttcg 58  
  
 <210> 61  
 <211> 21  
 <212> DNA  
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 <223> primer useful for amplifying from codon 485 to the translation  
 termination site at codon 933 of hMLH2  
  
 <400> 61  
 aaaacaagtc agtgaatcct c 21  
  
 <210> 62  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> 3' primer useful for amplifying up to codon 369 of hMLH2  
  
 <400> 62  
 aagcacatct gtttctgctg 20  
  
 <210> 63  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> 3' primer useful for amplifying up to codon 290 of hMLH2  
  
 <400> 63  
 acgagtagat tcctttaggc 20

<210> 64  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' primer useful for amplifying up to codon 214 of hMLH2

<400> 64  
cagaactgac atgagagcc 19

<210> 65  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 1 to 863 hMLH3

<400> 65  
ggatcctaatac gactcact atagggagac caccatggag cgagctgaga gc 52

<210> 66  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 1 to 863 hMLH3

<400> 66  
aggtagtagga agactctgtc 20

<210> 67  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying up to codon 472 of hMLH3

<400> 67  
ctgaggtctc agcaggc 17

<210> 68  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 415 to 863 of hMLH3

<400> 68  
ggatcctaatac gactcact atagggagac caccatgggtg tccattttcca gactgcg 57

<210> 69  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 415 to 863 of hMLH3

<400> 69  
aggttagtga agactctgtc

20

<210> 70  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 195 to 233 of hMLH2

<400> 70  
ttatttgga gaaaagcaga g

21

<210> 71  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 195 to 233 of hMLH2

<400> 71  
ttaaagact aacctcttgc c

21

<210> 72  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequencing primer useful for sequencing codons 195 to 233 of hMLH2

<400> 72  
ctgctgttat gaacaatatg g

21

<210> 73  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 233 to 257 of hMLH3

<400> 73

cagaagcagt tgcaaagcc  
19

<210> 74  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 233 to 257 of hMLH3

<400> 74  
aaaccgtact cttcacacac 20

<210> 75  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 347 of 377 of hMLH3

<400> 75  
gaggaaaagc ttttgttggc 20

<210> 76  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 347 of 377 of hMLH3

<400> 76  
cagtggctgc tgactgac 18

<210> 77  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 439 to 472 of hMLH3

<400> 77  
tccagaacca agaaggagc 19

<210> 78  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer useful for amplifying codons 439 to 472 of hMLH3

<400> 78  
tgaggtctca gcaggc

16

AK

20